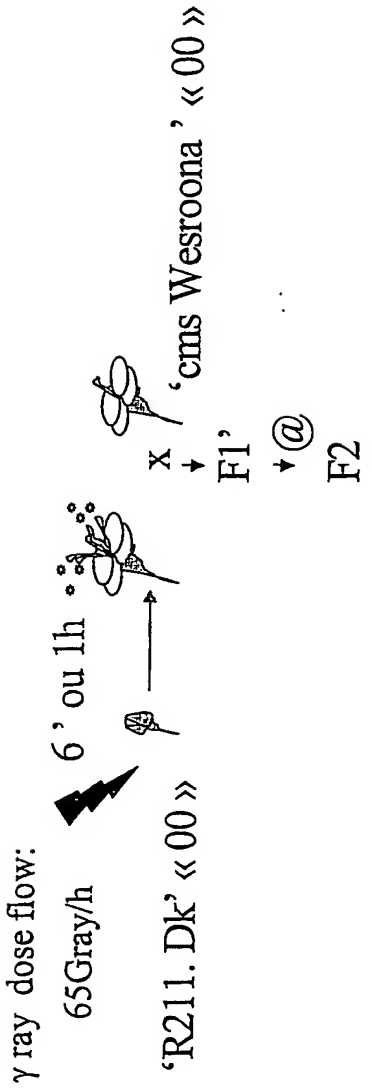

γ ray dose flow:
65Gray/h
6 ' ou 1h
'R211. Dk' « 00 »
x
'cms Wesroona ' « 00 »
F1'
@
F2

Fig 1

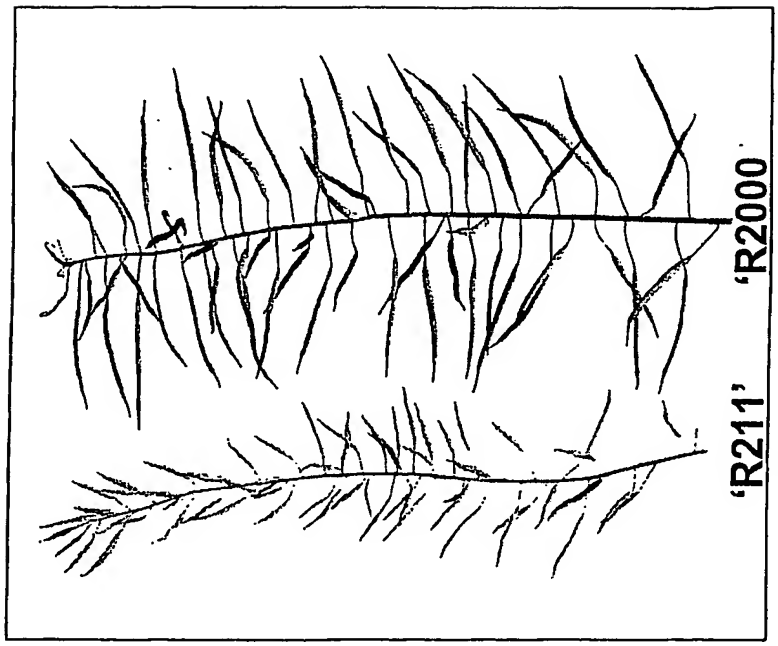


Fig. 1: Seed set on 'R211' and 'R2000'

Fig 2

Genotype	Selfings	Test Crosses
Drakkar	29.3	
Pactol	23.1	
R211	11.2	25.5
R2000	**26. 5** (24.0 – 31.1)	**27.0** (24.0 – 28.7)

Fig 3

Fig 4

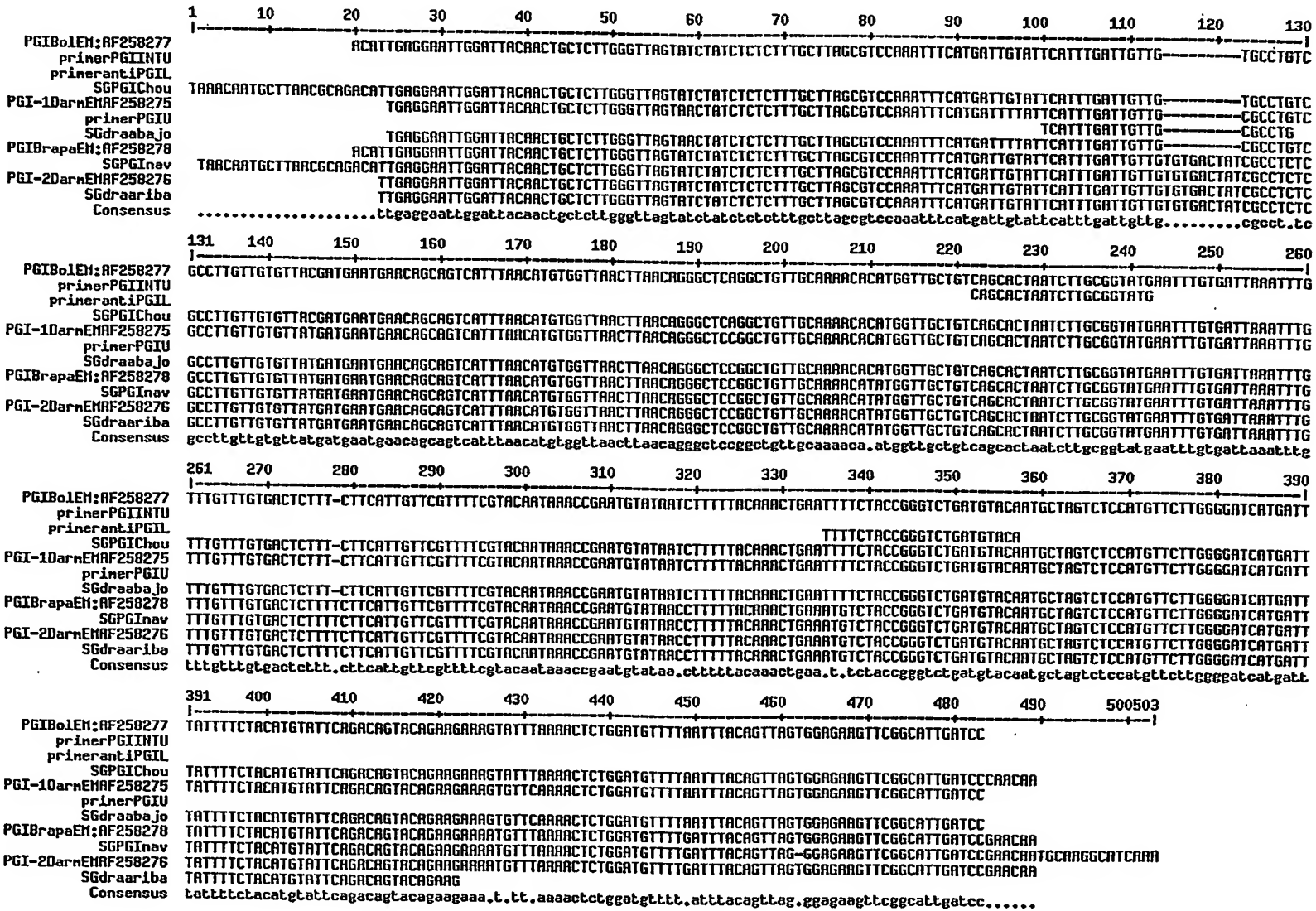
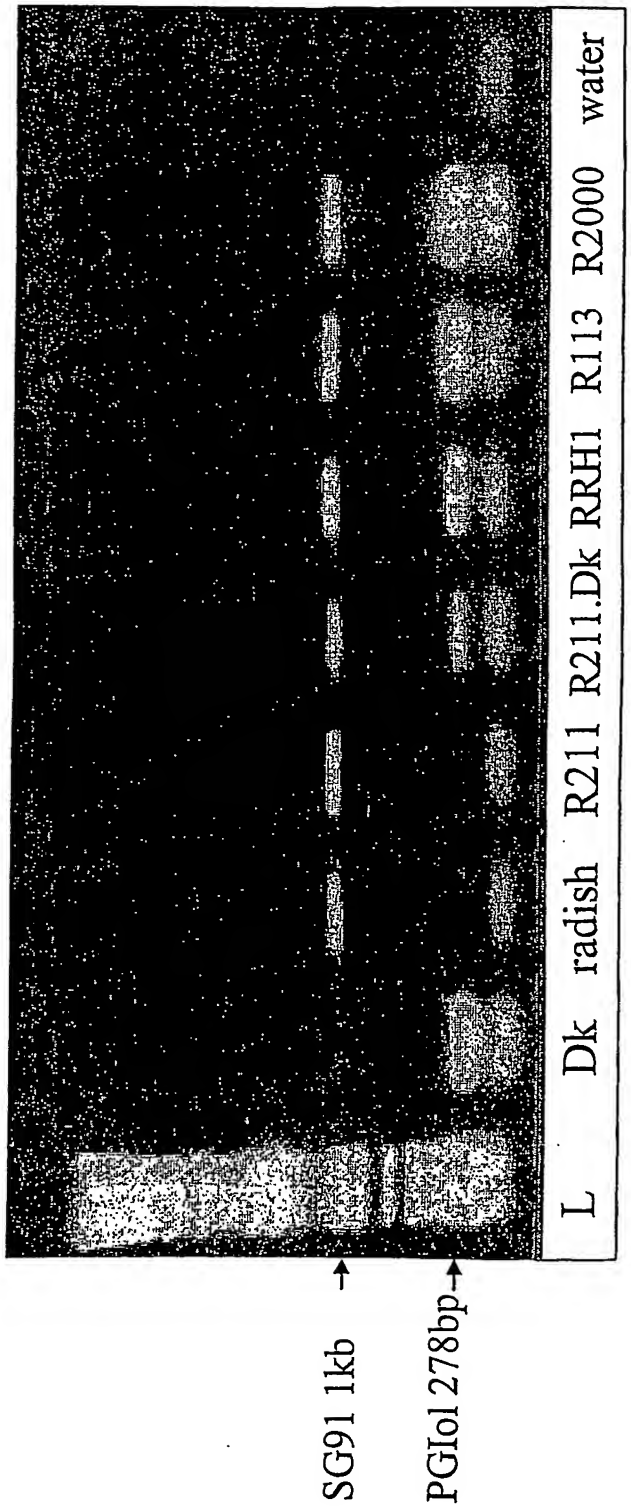
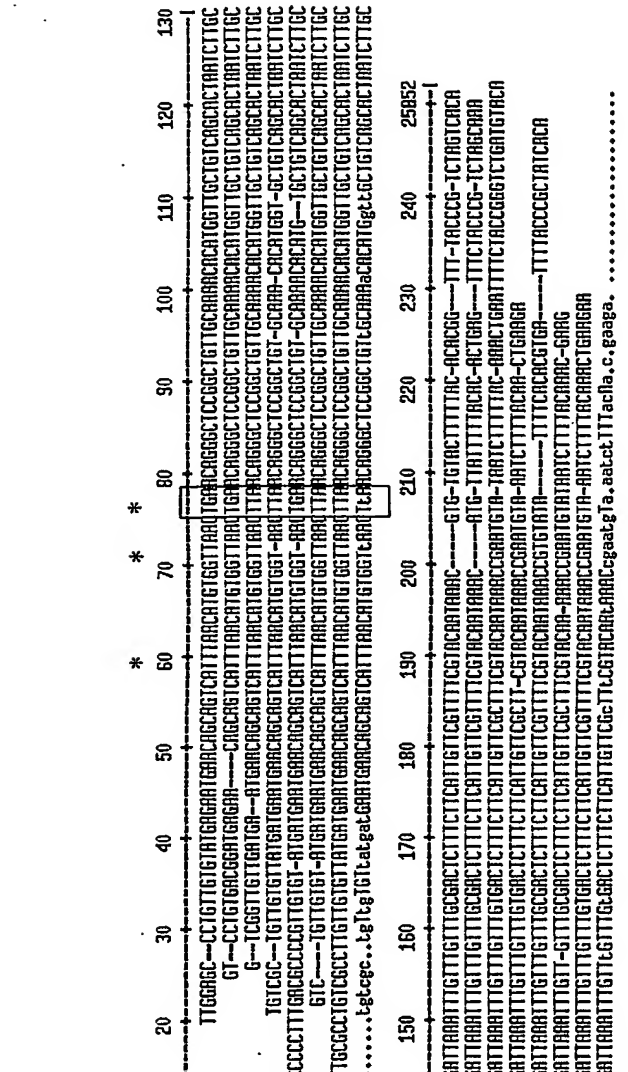

PGIBolEM:AF258277
primerPGIINTU
primerantiPGIL
SGPGIChou
PGI-1DarnEMAF258275
primerPGIU
SGdraabajo
PGIBrapaEM:AF258278
SGPGInav
PGI-2DarnEMAF258276
SGdraariba
Consensus

Fig 5



BEST AVAILABLE COPY

Fig 6



Msel restriction enzyme cut DNA sequences at the T/TAA sites (*)

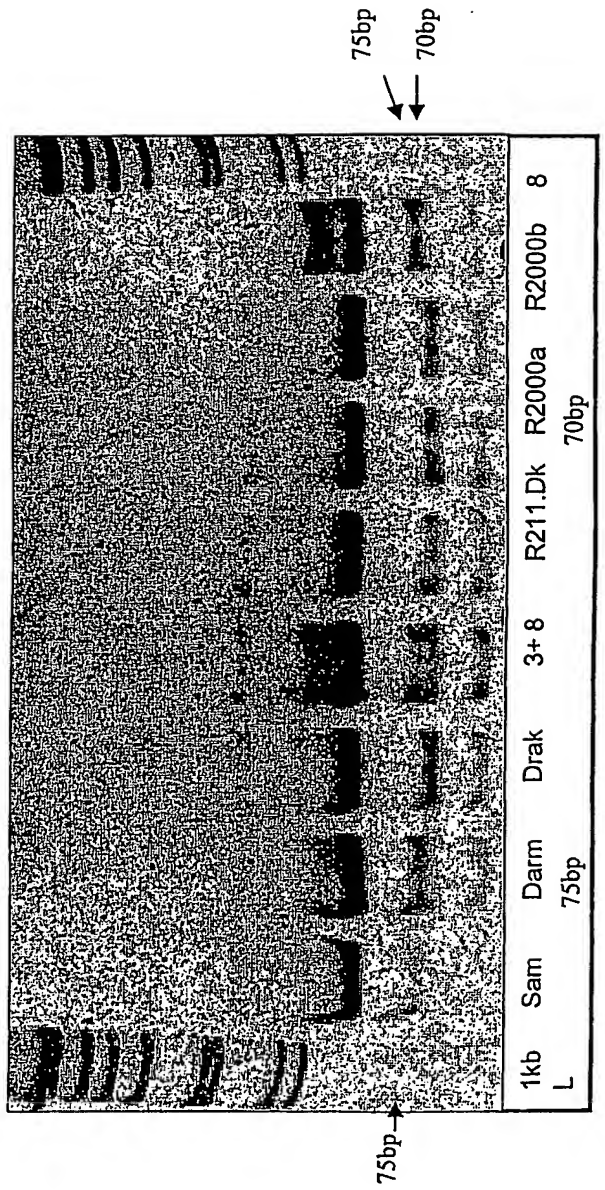
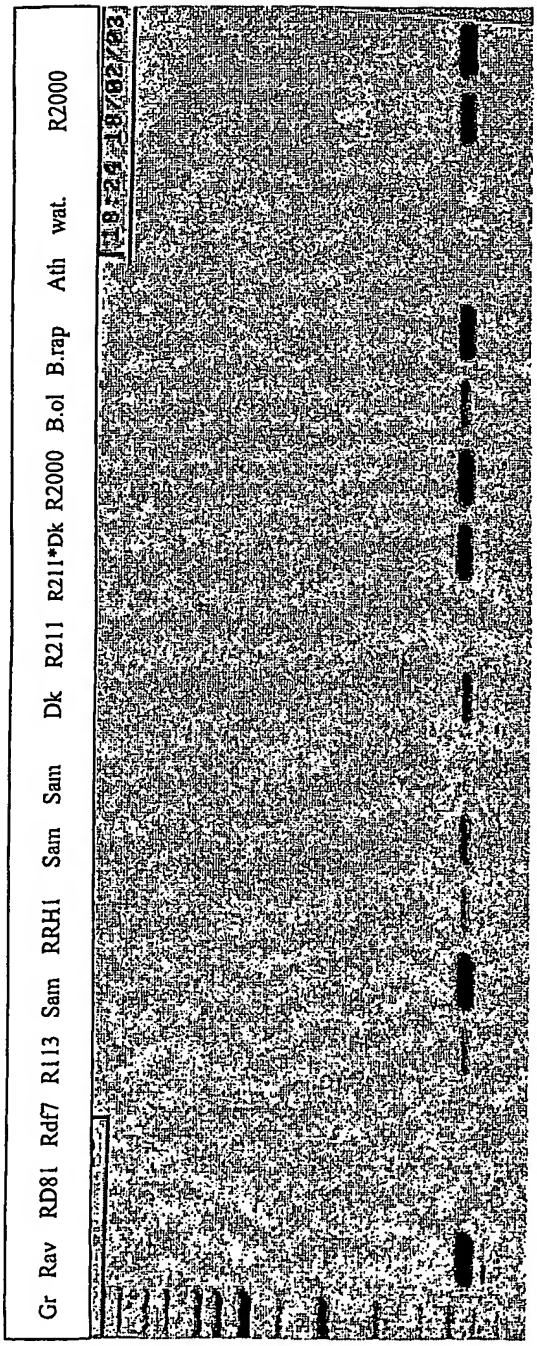


Fig 7

BEST AVAILABLE COPY

Fig 8



BEST AVAILABLE COPY

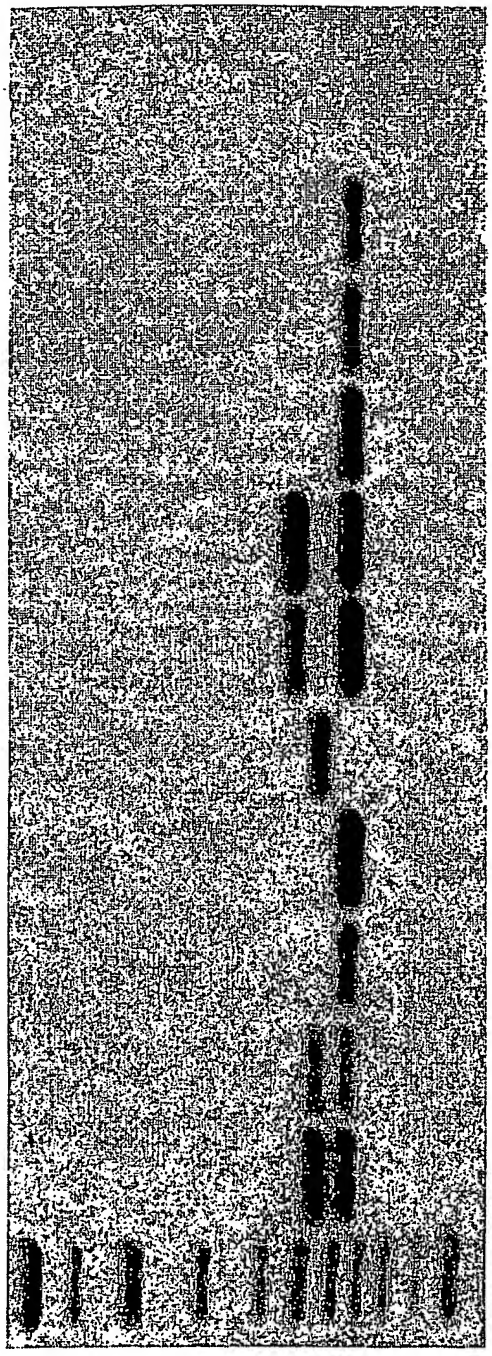
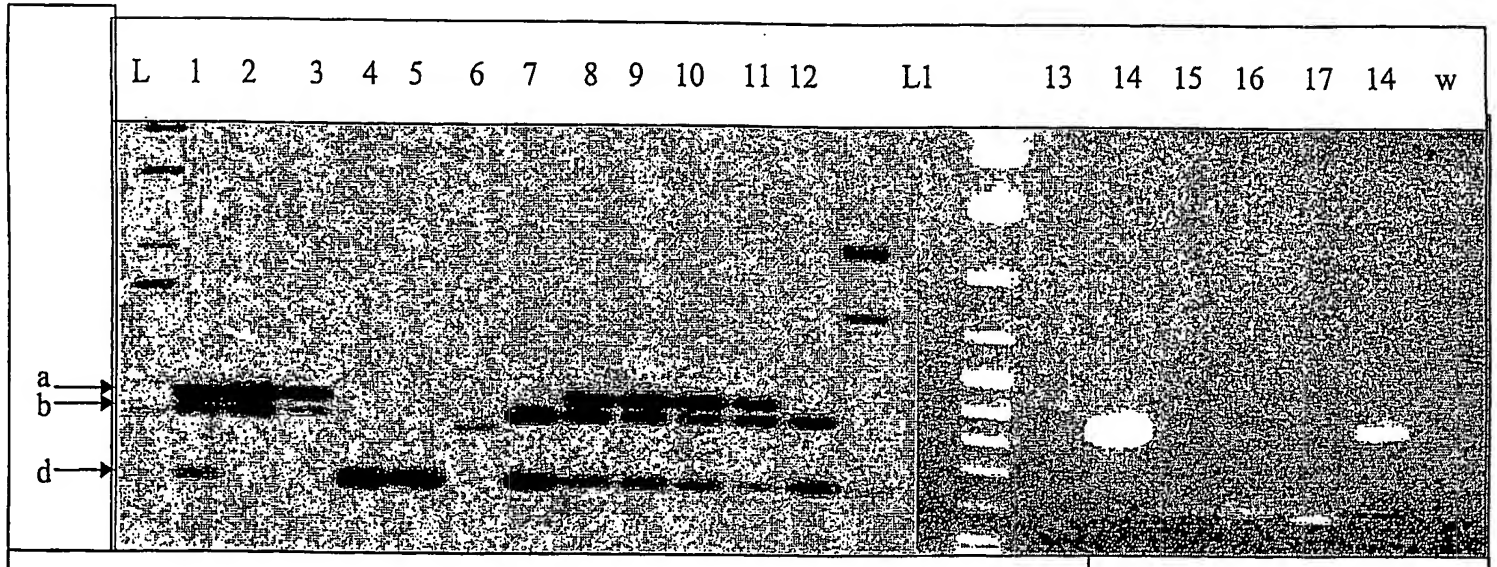


Fig 9

BEST AVAILABLE COPY

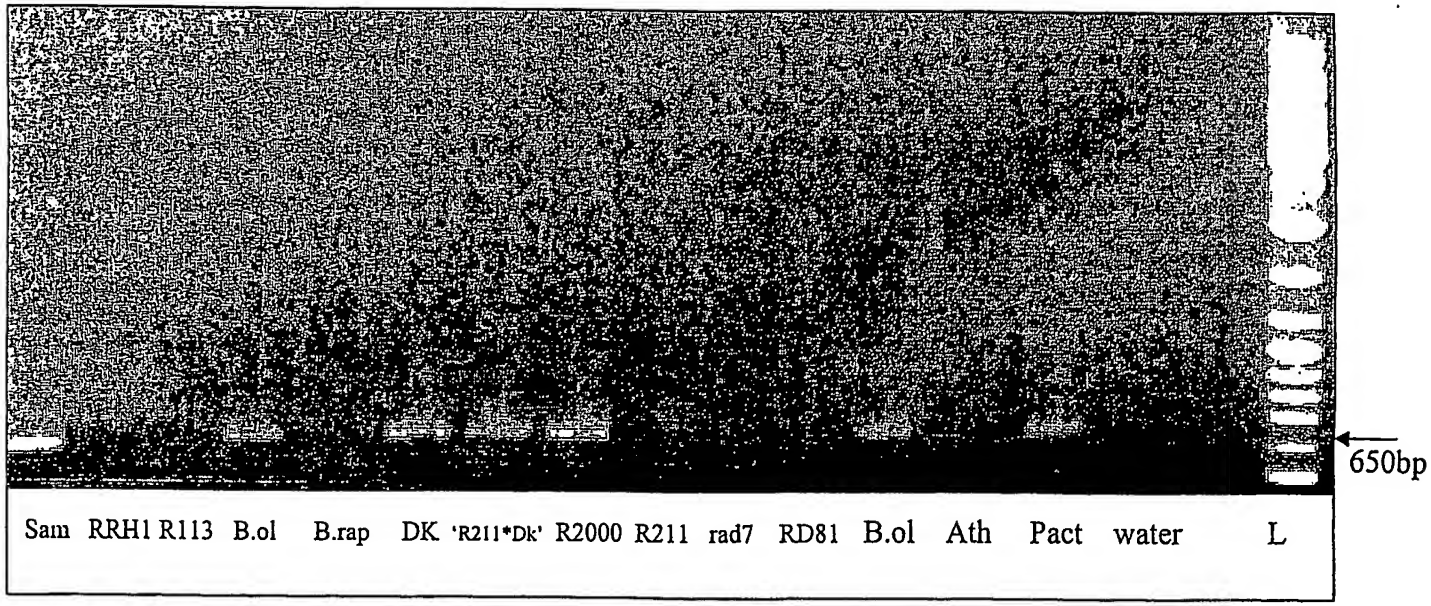
Fig 10



BolJon PCR bands (bp) n°		a	b	c	d	e
4,5	radish species:line 7				600	
17	radish RD81					590
14	B.rapa species		870			
13	B.oleracea species	950				
6	Arabidopsis thaliana (WS)			800		
2, 3	maintainer rapeseed: 2 Samourai; 3 Pactol	950	870			
7,12	homozygous restored rapeseed: 7 Samourai RRH1, 12 R211	0	870		600	
11	incomplete restored SRfi	950	870		600	
1,8	heterozygous restored rapeseed: R211.Dk	950	870		600	
9,10	homozygous restored R2000: 6 lineE38, 8,18,19 line R1.15	950	870		600	
L , L1	ladder1kb+, Ladder 100bp					

BEST AVAILABLE COPY

Fig 11



The CP418 band (about 650bp) specific to the B.oleracea genome.
It is present in B.ol, B.napus (Samourai, Drakkar, Pactol and the herterozygous R211*Dk)
It is absent from the restored rapeseed (RRH, R113 and R211)
It is present in the homozygous R2000.

BEST AVAILABLE COPY

Figure 12

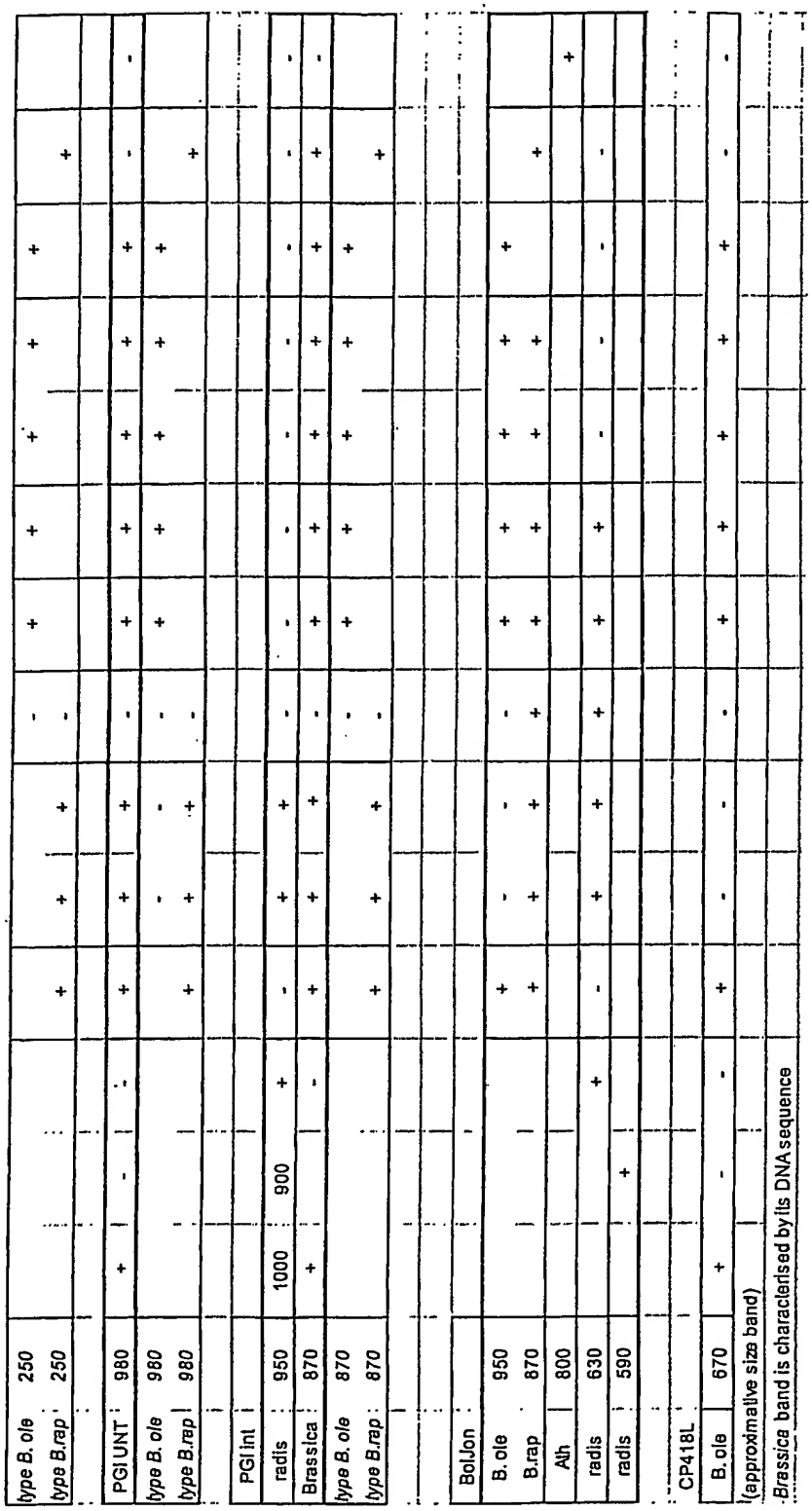

type B. ole 250
type B.rap 250
PGI UNT 980
type B. ole 980
type B.rap 980
PGI int
radis 950
Brassica 870
type B. ole 870
type B.rap 870
BolJon
B. ole 950
B.rap 870
Ath 800
radis 630
radis 590
CP418L
B. ole 670
(approximative size band)
-Brassica band is characterised by its DNA sequence

Figure 13 (a)

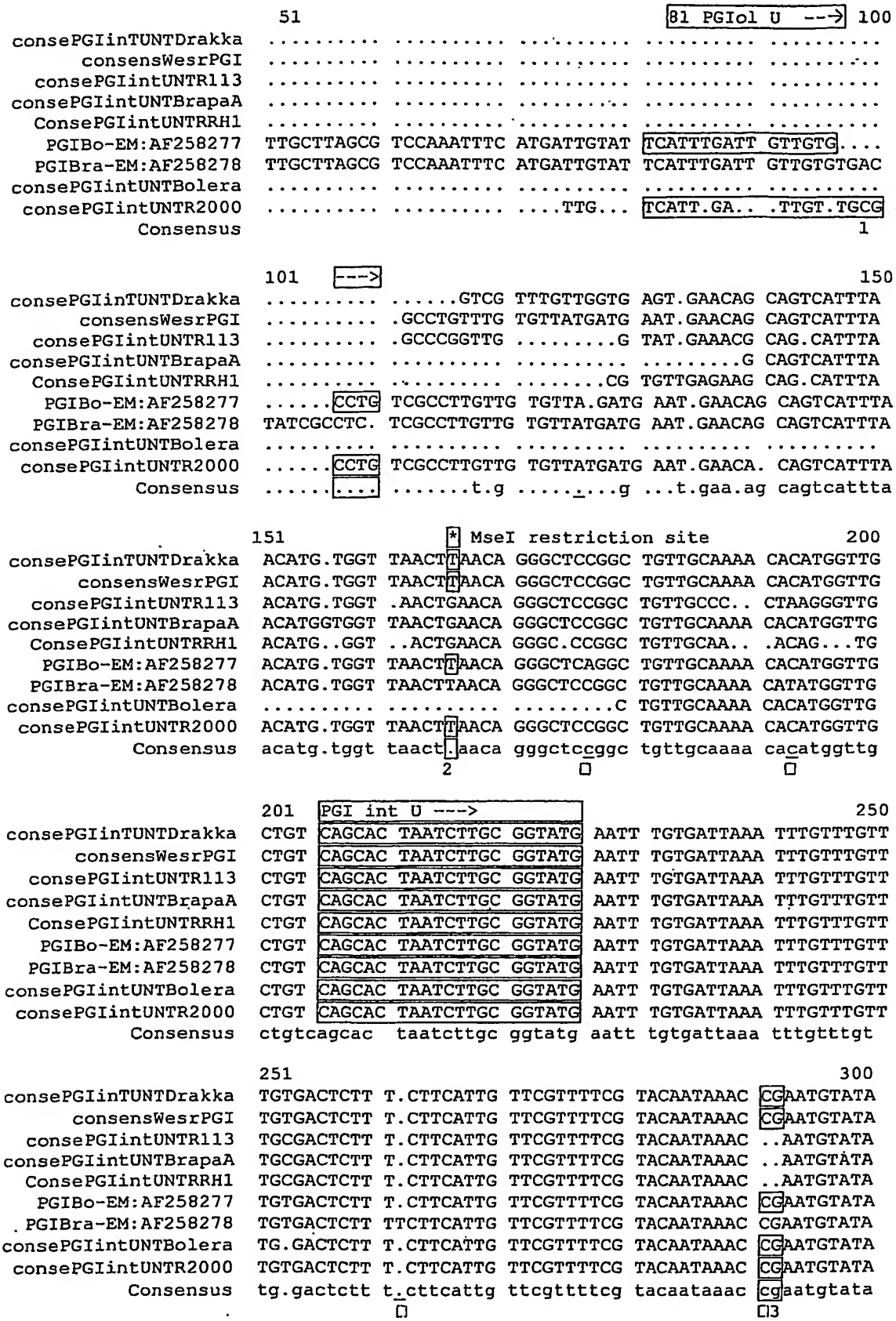

51
81 PGIol U --> 100
consePGIinTUNTDrakka
consensWesrPGI
consePGIintUNTR113
consePGIintUNTBrapaA
ConsePGIintUNTRRH1
PGIBo-EM:AF258277 TTGCTTAGCG TCCAAATTTC ATGATTGTAT TCATTTGATT GTTGTG....
PGIBra-EM:AF258278 TTGCTTAGCG TCCAAATTTC ATGATTGTAT TCATTTGATT GTTGTGTGAC
consePGIintUNTBolera
consePGIintUNTR2000
Consensus
101 --->
150
consePGIinTUNTDrakka ....GTCG TTTGTTGGTG AGT.GAACAG CAGTCATTTA
consensWesrPGI ..... .GCCTGTTTG TGTTATGATG AAT.GAACAG CAGTCATTTA
consePGIintUNTR113 ..... .GCCCGGTTG .....G TAT.GAAACG CAG.CATTTA
consePGIintUNTBrapaA ....G CAGTCATTTA
ConsePGIintUNTRRH1 ....CG TGTTGAGAAG CAG.CATTTA
PGIBo-EM:AF258277 .....CCTG TCGCCTTGTTG TGTTA.GATG AAT.GAACAG CAGTCATTTA
PGIBra-EM:AF258278 TATCGCCTC. TCGCCTTGTTG TGTTATGATG AAT.GAACAG CAGTCATTTA
consePGIintUNTBolera
consePGIintUNTR2000 .....CCTG TCGCCTTGTTG TGTTATGATG AAT.GAACA. CAGTCATTTA
Consensus .....CCTG .....t.g .....g ...t.gaa.ag cagtcattta
151
* MseI restriction site
200
consePGIinTUNTDrakka ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
consensWesrPGI ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
consePGIintUNTR113 ACATG.TGGT .AACTGAACA GGGCTCCGGC TGTTGCCC.. CTAAGGGTTG
consePGIintUNTBrapaA ACATGGTGGT TAACTGAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
ConsePGIintUNTRRH1 ACATG..GGT ..ACTGAACA GGGC.CCGGC TGTTGCAA.. .ACAG...TG
PGIBo-EM:AF258277 ACATG.TGGT TAACTTAACA GGGCTCAGGC TGTTGCAAAA CACATGGTTG
PGIBra-EM:AF258278 ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CATATGGTTG
consePGIintUNTBolera ....C TGTTGCAAAA CACATGGTTG
consePGIintUNTR2000 ACATG.TGGT TAACTTAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
Consensus acatg.tggt taact.aaca gggctccggc tgttgcaaaa cacatggttg
2
201
PGI int U --->
250
consePGIinTUNTDrakka CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consensWesrPGI CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTR113 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTBrapaA CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
ConsePGIintUNTRRH1 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
PGIBo-EM:AF258277 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
PGIBra-EM:AF258278 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTBolera CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTR2000 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
Consensus ctgtcagcac taatcttgc ggtatg aatt tgtgattaaa tttgtttgt
251
300
consePGIinTUNTDrakka TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
consensWesrPGI TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTR113 TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA
consePGIintUNTBrapaA TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA
ConsePGIintUNTRRH1 TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA
PGIBo-EM:AF258277 TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
PGIBra-EM:AF258278 TGTGACTCTT TTCTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTBolera TG.GACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTR2000 TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
Consensus tg.gactctt t.cttcattg ttcgttttcg tacaataaac cgaatgtata
3

Figure 13 (b)

```
                    301                    <---   PGIol antL 341      350
consePGIintUNTDrakka ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
      consensWesrPGI ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
  consePGIintUNTR113 ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTBrapaA ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
  ConsePGIintUNTRRH1 ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
   PGIBo-EM:AF258277 ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
  PGIBra-EM:AF258278 ACCTTTTTAC AAACTGAA AT GTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTBolera ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
 consePGIintUNTR2000 ATCTTTT.AC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
           Consensus  atcttttac aaactgaa  tt ttctaccggg tctgatgtac a atgctAGTC
```

Figure 14 (a)

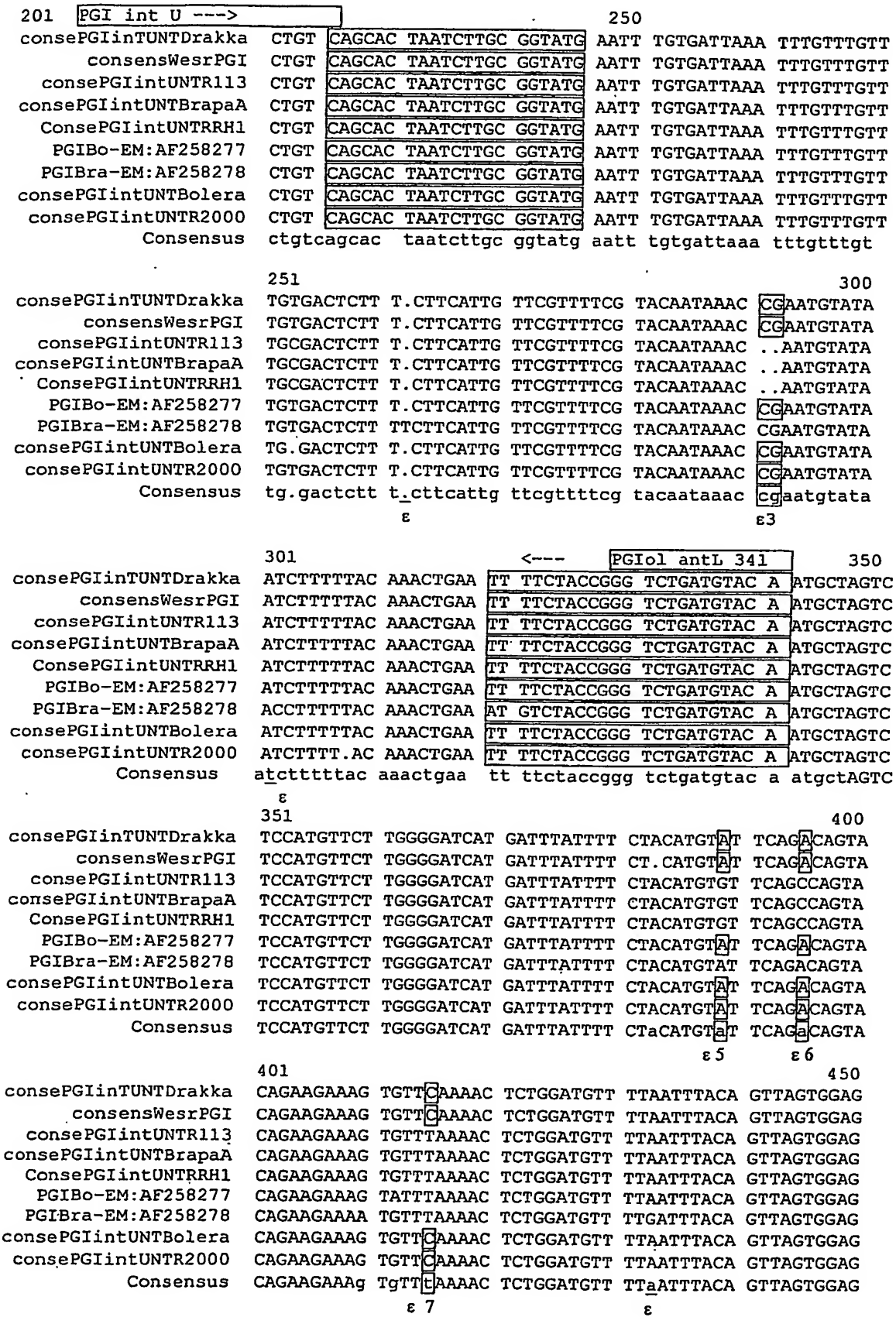

201 PGI int U ---> 250
consePGIinTUNTDrakka CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consensWesrPGI CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTR113 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTBrapaA CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
ConsePGIintUNTRRH1 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
PGIBo-EM:AF258277 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
PGIBra-EM:AF258278 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTBolera CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTR2000 CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTTGTT
Consensus ctgtcagcac taatcttgc ggtatg aatt tgtgattaaa tttgtttgt
251 300
consePGIinTUNTDrakka TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
consensWesrPGI TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTR113 TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA
consePGIintUNTBrapaA TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA
ConsePGIintUNTRRH1 TGCGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC ..AATGTATA
PGIBo-EM:AF258277 TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
PGIBra-EM:AF258278 TGTGACTCTT TTCTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTBolera TG.GACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTR2000 TGTGACTCTT T.CTTCATTG TTCGTTTTCG TACAATAAAC CGAATGTATA
Consensus tg.gactctt t.cttcattg ttcgttttcg tacaataaac cgaatgtata
ε ε3
301 <--- PGIol antL 341 350
consePGIinTUNTDrakka ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consensWesrPGI ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTR113 ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTBrapaA ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
ConsePGIintUNTRRH1 ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
PGIBo-EM:AF258277 ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
PGIBra-EM:AF258278 ACCTTTTTAC AAACTGAA AT GTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTBolera ATCTTTTTAC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
consePGIintUNTR2000 ATCTTTT.AC AAACTGAA TT TTCTACCGGG TCTGATGTAC A ATGCTAGTC
Consensus atcttttac aaactgaa tt ttctaccggg tctgatgtac a atgctAGTC
ε
351 400
consePGIinTUNTDrakka TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
consensWesrPGI TCCATGTTCT TGGGGATCAT GATTTATTTT CT.CATGTAT TCAGACAGTA
consePGIintUNTR113 TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTGT TCAGCCAGTA
consePGIintUNTBrapaA TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTGT TCAGCCAGTA
ConsePGIintUNTRRH1 TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTGT TCAGCCAGTA
PGIBo-EM:AF258277 TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
PGIBra-EM:AF258278 TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
consePGIintUNTBolera TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
consePGIintUNTR2000 TCCATGTTCT TGGGGATCAT GATTTATTTT CTACATGTAT TCAGACAGTA
Consensus TCCATGTTCT TGGGGATCAT GATTTATTTT CTaCATGTaT TCAGaCAGTA
ε5 ε6
401 450
consePGIinTUNTDrakka CAGAAGAAAG TGTTCAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
consensWesrPGI CAGAAGAAAG TGTTCAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
consePGIintUNTR113 CAGAAGAAAG TGTTTAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
consePGIintUNTBrapaA CAGAAGAAAG TGTTTAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
ConsePGIintUNTRRH1 CAGAAGAAAG TGTTTAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
PGIBo-EM:AF258277 CAGAAGAAAG TATTTAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
PGIBra-EM:AF258278 CAGAAGAAAA TGTTTAAAAC TCTGGATGTT TTGATTTACA GTTAGTGGAG
consePGIintUNTBolera CAGAAGAAAG TGTTCAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
consePGIintUNTR2000 CAGAAGAAAG TGTTCAAAAC TCTGGATGTT TTAATTTACA GTTAGTGGAG
Consensus CAGAAGAAAg TgTTtAAAAC TCTGGATGTT TTaATTTACA GTTAGTGGAG
ε 7 ε

Figure 14 (b)

```
                        451          end of Data Base PGI sequences          500
consePGIinTUNTDrakka    AAGTTCGGCA TTGATCCGAA CAATGCATTT GCATTTTGGG ACTGGGTTGG
      consensWesrPGI    AAGTTCGGCA TTGATCCGAA CAATGCATTT GCATTTTGGG ACTGGGTTGG
  consePGIintUNTR113    AAGTTCGGCA TTGATCCGAA CAATGCATTT GCATTTTGGG ACTGGGTTGG
consePGIintUNTBrapaA    AAGTTCGGCA TTGATCCGAA CAATGCATTT GCATTTTGGG ACTGGGTTGG
  ConsePGIintUNTRRH1    AAGTTCGGCA TTGATCCGAA CAATGCATTT GCATTTTGGG ACTGGGTTGG
   PGIBo-EM:AF258277    AAGTTCGGCA TTGATCC... .......... .......... ..........
   PGIBra-EM:AF258278   AAGTTCGGCA TTGATCCGAA CAA....... .......... ..........
consePGIintUNTBolera    AAGTTCGGCA TTGATCCGAA CAATGCATTT GCATTTTGGG ACTGGGTTGG
 consePGIintUNTR2000    AAGTTCGGCA TTGATCCGAA CAATGCATTT GCATTTTGGG ACTGGGTTGG
           Consensus    AAGTTCGGCA TTGATCCgaa caatgcattt gcattttggg actgggttgg

                        501                                                 550
consePGIinTUNTDrakka    TGGAAGGTAC AGTGGTAAGT GCTTGTTTAT TTGGTTGTAT AAATTTCTCG
      consensWesrPGI    TGGAAGGTAC AGTGGTAAGT GCTTGTTTAT TTGGTTGTAT AAATTTCTCG
  consePGIintUNTR113    TGGAAGGTAC AGTGGTAAGT GCTTGTTTAT TTGGTTGTAT TAATTTCTCA
consePGIintUNTBrapaA    TGGAAGGTAC AGTGGTAAGT GCTTGTTTAT TTGGTTGTAT TAATTTCTCA
  ConsePGIintUNTRRH1    TGGAAGGTAC AGTGGTAAGT GCTTGTTTAT TTGGTTGTAT TAATTTCTCA
   PGIBo-EM:AF258277    .......... .......... .......... .......... ..........
   PGIBra-EM:AF258278   .......... .......... .......... .......... ..........
consePGIintUNTBolera    TGGAAGGTAC AGTGGTAAGT GCTTGTTTAT TTGGTTGTAT AAATTTCTCG
 consePGIintUNTR2000    TGGAAGGTAC AGTGGTAAGT GCTTGTTTAT TTGGTTGTAT AAATTTCTCG
           Consensus    tggaaggtac agtggtaagt gcttgtttat ttggttgtat .aatttctc.
                                                                    8         9
                        551                                                 600
consePGIinTUNTDrakka    TCCATTTCCG CTTGCTTAGT GTATAACTGA AATTCTTTTG CAGTTTGCAG
      consensWesrPGI    TCCATTTCCG CTTGCTTAGT GTATAACTGA AATTCTTTTG CAGTTTGCAG
  consePGIintUNTR113    TCCATATCCG CTTGCTTAGT TTATAACTGA AATTCTTTTG CAGTTTGCAG
consePGIintUNTBrapaA    TCCATATCCG CTTGCTTAGT TTATAACTGA AATTCTTTTG CAGTTTGCAG
  ConsePGIintUNTRRH1    TCCATATCCG CTTGCTTAGT TTATAACTGA AATTCTTTTG CAGTTTGCAG
   PGIBo-EM:AF258277    .......... .......... .......... .......... ..........
   PGIBra-EM:AF258278   .......... .......... .......... .......... ..........
consePGIintUNTBolera    TCCATTTCCG CTTGCTTAGT GTATAACTGA AATTCTTTTG CAGTTTGCAG
 consePGIintUNTR2000    TCCATTTCCG CTTGCTTAGT GTATAACTGA AATTCTTTTG CAGTTTGCAG
           Consensus    tccat.tccg cttgcttagt .tataactga aattcttttg cagtttgcag
                             10                  11
                        601                                                 650
consePGIinTUNTDrakka    TGCTGTTGGA GTCTTACCAT TGTCTCTACA GTATGGCTTC TCTGTGGTTG
      consensWesrPGI    TGCTGTTGGA GTCTTACCAT TGTCTCTACA GTATGGCTTC TCTGTGGTTG
  consePGIintUNTR113    TGCTGTTGGA GTCTTACCAT TGTCTCTACA GTATGGCTTC TCCGTGGTTG
consePGIintUNTBrapaA    TGCTGTTGGA GTCTTACCAT TGTCTCTACA GTATGGCTTC TCCGTGGTTG
  ConsePGIintUNTRRH1    TGCTGTTGGA GTCTTACCAT TGTCTCTACA GTATGGCTTC TCCGTGGTTG
   PGIBo-EM:AF258277    .......... .......... .......... .......... ..........
   PGIBra-EM:AF258278   .......... .......... .......... .......... ..........
consePGIintUNTBolera    TGCTGTTGGA GTCTTACCAT TGTCTCTACA GTATGGCTTC TCTGTGGTTG
 consePGIintUNTR2000    TGCTGTTGGA GTCTTACCAT TGTCTCTACA GTATGGCTTC TCTGTGGTTG
           Consensus    tgctgttgga gtcttaccat tgtctctaca gtatggcttc tc.gtggttg
                                                                      12
                        651                                                 700
consePGIinTUNTDrakka    AGAAGTACGG TACCTTCTAC TTTATCAGCC ATCTCATAAA ATGTCTTAGG
      consensWesrPGI    AGAAGTACGG TACCTTCTAC TTTATCAGCC ATCTCATAAA ATGTCTTAGG
  consePGIintUNTR113    AGAAGTACGG TACCTTCTAC TTTATTAGCC ATCTCATAAA ATGTCTTGGG
consePGIintUNTBrapaA    AGAAGTACGG TACCTTCTAC TTTATTAGCC ATCTCATAAA ATGTCTTGGG
  ConsePGIintUNTRRH1    AGAAGTACGG TACCTTCTAC TTTATTAGCC ATCTCATAAA ATGTCTTGGG
   PGIBo-EM:AF258277    .......... .......... .......... .......... ..........
   PGIBra-EM:AF258278   .......... .......... .......... .......... ..........
consePGIintUNTBolera    AGAAGTACGG TACCTTCTAC TTTATCAGCC ATCTCATAAA A.GTCTTAGG
 consePGIintUNTR2000    AGAAGTACGG TACCTTCTAC TTTATCAGCC ATCTCATAAA ATGTCTTAGG
           Consensus    agaagtacgg taccttctac tttat.agcc atctcataaa atgtctt.gg
                                               13                        14
```

Figure 14 (c)

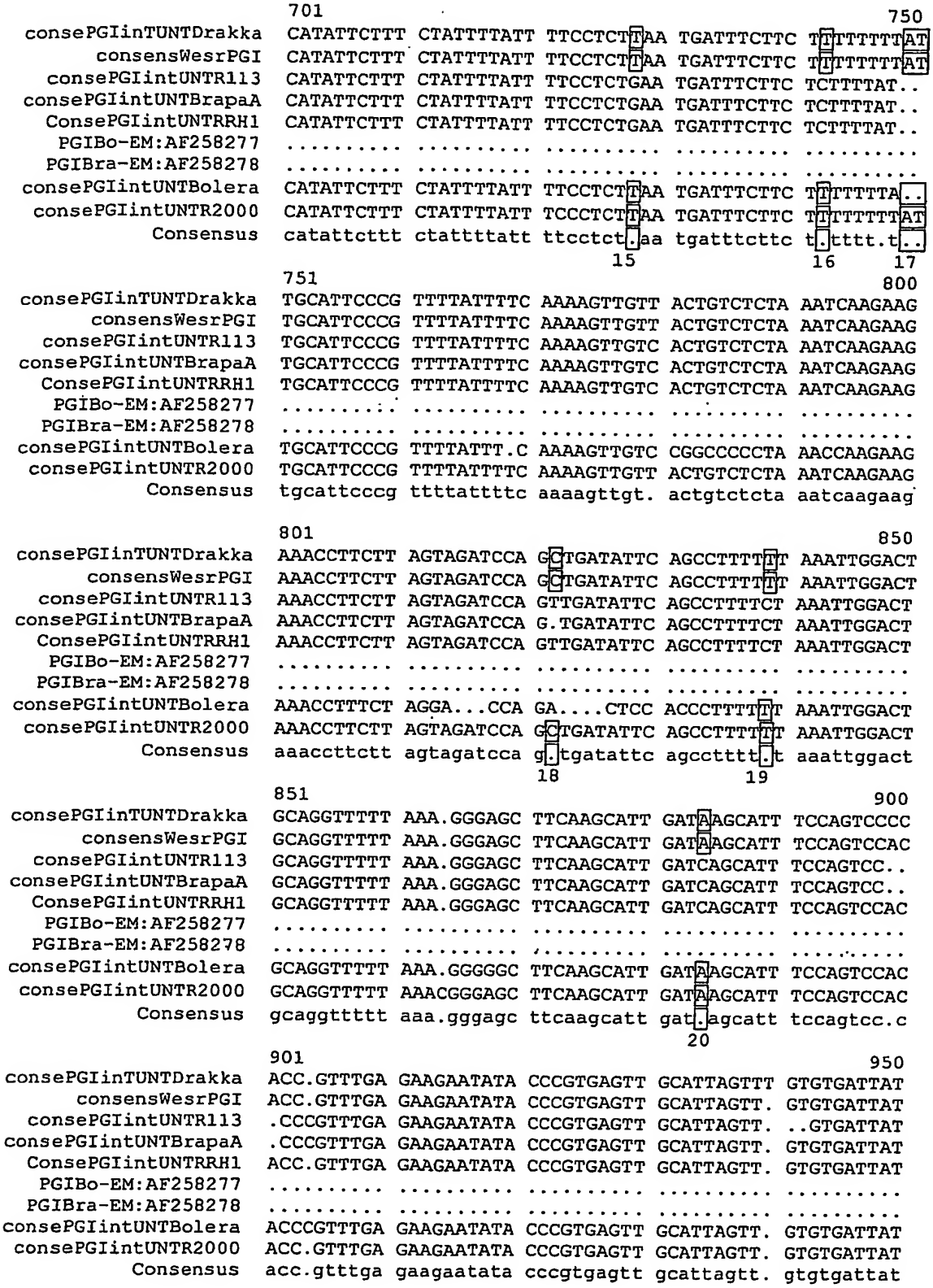

701 750
consePGIinTUNTDrakka CATATTCTTT CTATTTTATT TTCCTCTTAA TGATTTCTTC TTTTTTTTAT
consensWesrPGI CATATTCTTT CTATTTTATT TTCCTCTTAA TGATTTCTTC TTTTTTTTAT
consePGIintUNTR113 CATATTCTTT CTATTTTATT TTCCTCTGAA TGATTTCTTC TCTTTTAT..
consePGIintUNTBrapaA CATATTCTTT CTATTTTATT TTCCTCTGAA TGATTTCTTC TCTTTTAT..
ConsePGIintUNTRRH1 CATATTCTTT CTATTTTATT TTCCTCTGAA TGATTTCTTC TCTTTTAT..
PGIBo-EM:AF258277 ....
PGIBra-EM:AF258278 ....
consePGIintUNTBolera CATATTCTTT CTATTTTATT TTCCTCTTAA TGATTTCTTC TTTTTTTA..
consePGIintUNTR2000 CATATTCTTT CTATTTTATT TCCCTCTTAA TGATTTCTTC TTTTTTTTAT
Consensus catattcttt ctattttatt ttcctct.aa tgatttcttc t.tttt.t..
15 16 17
751 800
consePGIinTUNTDrakka TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG
consensWesrPGI TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG
consePGIintUNTR113 TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG
consePGIintUNTBrapaA TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG
ConsePGIintUNTRRH1 TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG
PGIBo-EM:AF258277 ....
PGIBra-EM:AF258278 ....
consePGIintUNTBolera TGCATTCCCG TTTTATTT.C AAAAGTTGTC CGGCCCCCTA AACCAAGAAG
consePGIintUNTR2000 TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG
Consensus tgcattcccg ttttattttc aaaagttgt. actgtctcta aatcaagaag
801 850
consePGIinTUNTDrakka AAACCTTCTT AGTAGATCCA GCTGATATTC AGCCTTTTTT AAATTGGACT
consensWesrPGI AAACCTTCTT AGTAGATCCA GCTGATATTC AGCCTTTTTT AAATTGGACT
consePGIintUNTR113 AAACCTTCTT AGTAGATCCA GTTGATATTC AGCCTTTTCT AAATTGGACT
consePGIintUNTBrapaA AAACCTTCTT AGTAGATCCA G.TGATATTC AGCCTTTTCT AAATTGGACT
ConsePGIintUNTRRH1 AAACCTTCTT AGTAGATCCA GTTGATATTC AGCCTTTTCT AAATTGGACT
PGIBo-EM:AF258277 ....
PGIBra-EM:AF258278 ....
consePGIintUNTBolera AAACCTTTCT AGGA...CCA GA....CTCC ACCCTTTTTT AAATTGGACT
consePGIintUNTR2000 AAACCTTCTT AGTAGATCCA GCTGATATTC AGCCTTTTTT AAATTGGACT
Consensus aaaccttctt agtagatcca g.tgatattc agcctttt.t aaattggact
18 19
851 900
consePGIinTUNTDrakka GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAAGCATT TCCAGTCCCC
consensWesrPGI GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAAGCATT TCCAGTCCAC
consePGIintUNTR113 GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..
consePGIintUNTBrapaA GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..
ConsePGIintUNTRRH1 GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCCAC
PGIBo-EM:AF258277 ....
PGIBra-EM:AF258278 ....
consePGIintUNTBolera GCAGGTTTTT AAA.GGGGGC TTCAAGCATT GATAAGCATT TCCAGTCCAC
consePGIintUNTR2000 GCAGGTTTTT AAACGGGAGC TTCAAGCATT GATAAGCATT TCCAGTCCAC
Consensus gcaggttttt aaa.gggagc ttcaagcatt gat.agcatt tccagtcc.c
20
901 950
consePGIinTUNTDrakka ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTTT GTGTGATTAT
consensWesrPGI ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
consePGIintUNTR113 .CCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. ..GTGATTAT
consePGIintUNTBrapaA .CCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
ConsePGIintUNTRRH1 ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
PGIBo-EM:AF258277 ....
PGIBra-EM:AF258278 ....
consePGIintUNTBolera ACCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
consePGIintUNTR2000 ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
Consensus acc.gtttga gaagaatata cccgtgagtt gcattagtt. gtgtgattat

Figure 14 (d)

```
                        951                                                1000
consePGIinTUNTDrakka    ACAGTTTTTC TTGTCTTTTT GCTATGCCCA TCAACACTAG AAGATTCGTG
     consensWesrPGI     ACAGTTTT.C TTGTCTTTT. GCTATGTCCA TCAACACTAG A.GATTCGTG
consePGIintUNTR113      ACAGTTTT.C TTGCCTTTTT GCTAT..AGG GCAAC.CTAG A.GATTCATG
consePGIintUNTBrapaA    ACAGTTTT.C TTGTCTTTT. GCTATG.TCA TCAAC.CTAG A.GATTCATG
ConsèPGIintUNTRRH1      ACAGTTTT.C TTGTCTTTTT GCTAT...AT GCAACCCTAG ..GATTCATG
PGIBo-EM:AF258277       .......... .......... .......... .......... ..........
PGIBra-EM:AF258278      .......... .......... .......... .......... ..........
consePGIintUNTBolera    ACAGTTTT.C TTGTCTTTTT GCTAG..TGA TCAAC.CTAG A.GATTCGTG
consePGIintUNTR2000     ACAGTTTT.C TTGTCTTTTT GCTATGTCCA TCAACACTAG A.GATTCGTG
Consensus               acagtttt.c ttgtcttttt gctat....a tcaac.ctag a.gattc.tg
                                                                        21

                        1001                                               1050
consePGIinTUNTDrakka    AAGTTATTAG TGTAGCCAAC GCCTAGGGGG AGGTTGGTTG GCTGTTTTGG
     consensWesrPGI     AAGTTATTAG TGTAGTCAAC GCA..... .......... ..........
consePGIintUNTR113      AAGTTATTAG TGTAGTCAAC GCAGAGGAGA G..TTCACTG ACGG......
consePGIintUNTBrapaA    AAGTTATTAG TGTAGTCAAC GCAGAGTGAG AGG.TGATTG ..........
ConsePGIintUNTRRH1      AAGTTATTAG TGTAGTCAAC GCAGAGGAGG AGATGGTT.. ..........
PGIBo-EM:AF258277       .......... .......... .......... .......... ..........
PGIBra-EM:AF258278      .......... .......... .......... .......... ..........
consePGIintUNTBolera    AAGTTATTAG TGTAGTCAAC GCATAGGAGG AGC....... ..........
consePGIintUNTR2000     AAGTTATTAG TGTAGTCAAC GCATAGGGAG AGGTGAT.GG TGACTTTTGG
Consensus               aagttattag tgtagtcaac gca.agg.g. .g........ ..........

                        1051                    1076
consePGIinTUNTDrakka    ACGTTTTCAC GTGCTCCGGG GGGTTTTTGG GGACCAAACC CCCAAC
     consensWesrPGI     .......... .......... .......... .......... ......
consePGIintUNTR113      .......... .......... .......... .......... ......
consePGIintUNTBrapaA    .......... .......... .......... .......... ......
ConsePGIintUNTRRH1      .......... .......... .......... .......... ......
PGIBo-EM:AF258277       .......... .......... .......... .......... ......
PGIBra-EM:AF258278      .......... .......... .......... .......... ......
consePGIintUNTBolera    .......... .......... .......... .......... ......
consePGIintUNTR2000     ACGATTTCAG GTGCTTTAGG GTTATTG..... ..........
```

Figure 15 (a)

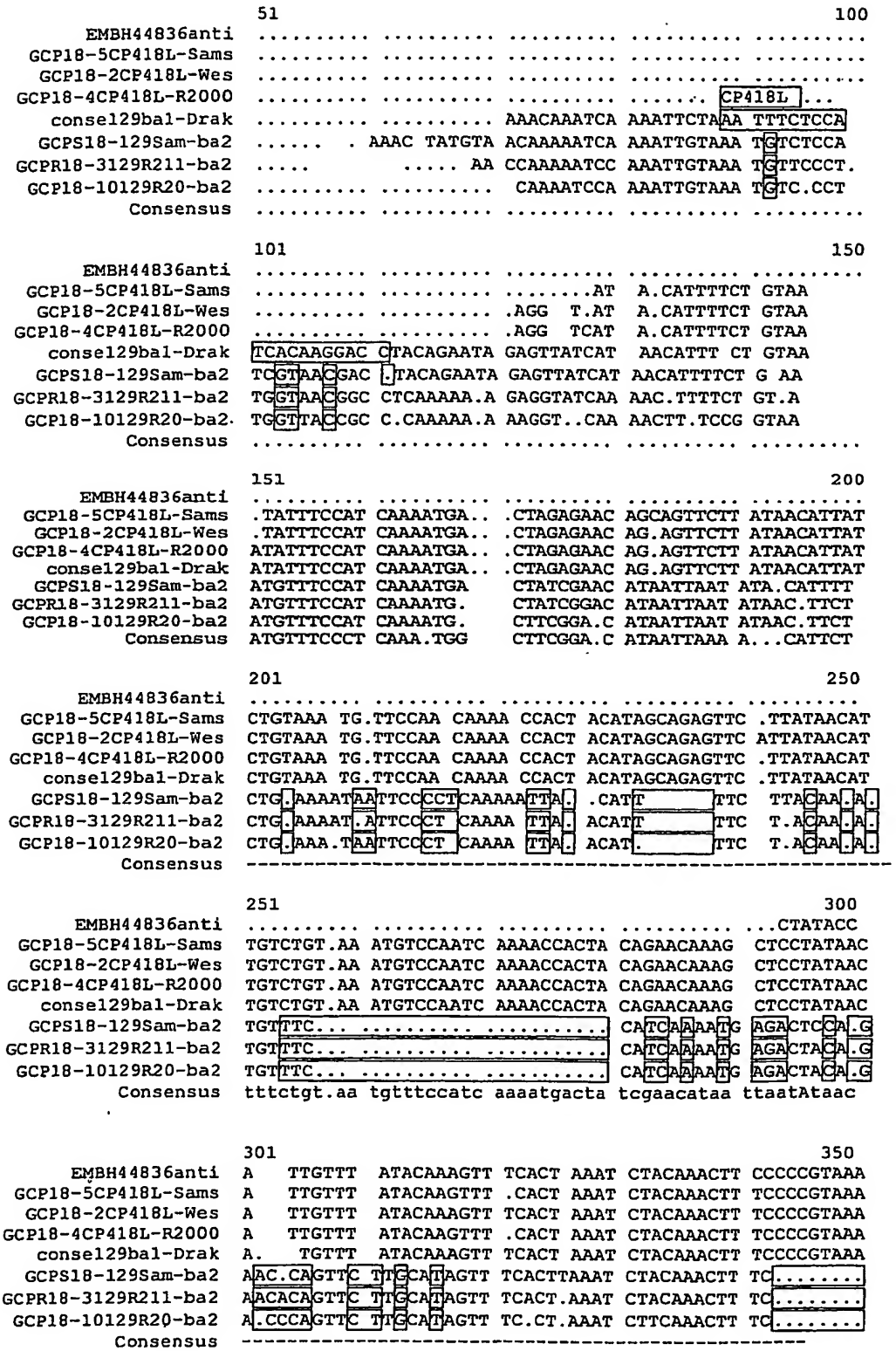

51 100
EMBH44836anti
GCP18-5CP418L-Sams
GCP18-2CP418L-Wes
GCP18-4CP418L-R2000
CP418L
conse129bal-Drak
GCPS18-129Sam-ba2
GCPR18-3129R211-ba2
GCP18-10129R20-ba2
Consensus
101 150
151 200
201 250
251 300
301 350

Figure 15 (b)

351
400
EMBH44836anti TGAGCTTAAT ATCACCCAA. GATGTTTCA ATCAGAT AAA GAGTAACGAC
GCP18-5CP418L-Sams TGAGCTTAAT ATCACCCAAA GATGTTTCA ATCAGAT AAA GAGTAACGAC
GCP18-2CP418L-Wes TGAGCTTAAT ATCACCCAAA GATGTTTCA ATCAGAT AAA GAGTAACGAC
GCP18-4CP418L-R2000 TGAGCTTAAT ATCACCCAAA GATGTTTCA ATCAGAT AAA GAGTAACGAC
consel29bal-Drak TGAGCTTAAT ATCACCCAAA GATGTTTCA ATCAGAT AAA GAGTA.CGAC
GCPS18-129Sam-ba2 .....AAT CTTATCTAAA G.TTATCAC ATCACAT GAA GA. .....
GCPR18-3129R211-ba2 .....AAT CTTATCTAA. G.TTATCAC ATCACAT GAA GA. .....
GCP18-10129R20-ba2 .....AAT CTTATCTAAA G.TTATCAC ATCACAT GAA GA. .....
Consensus
401
EMBH44836anti ATCGTTTTGA GATTAGAACA AA
GCP18-5CP418L-Sams ATCGTTTTGA GATTAGAACA AA
GCP18-2CP418L-Wes ATCGTTTTGA GATTAGAACA AA
GCP18-4CP418L-R2000 ATCGTTTTGA GATTAGAACA AA
consel29bal-Drak ATCGTTTTGA GATTAGAACA AA
GCPS18-129Sam-ba2 .... .GAGC AA
GCPR18-3129R211-ba2 ....GGC AA
GCP18-10129R20-ba2 ....GGC A.
Consensus
431
480
EMBH44836anti CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC
GCP18-5CP418L-Sams CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC
GCP18-2CP418L-Wes CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAG.
GCP18-4CP418L-R2000 CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC
consel29bal-Drak CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC
GCPS18-129Sam-ba2 GTAAAACCTTA CCTAGAGTGA TCTGAGGAGT AGGCTCGTTG CCAGCGGAGC
GCPR18-3129R211-ba2 GTAAAACCTTA CCTAGAGTGA TCTGAGGAGT AGGCTCGTTG CCAGCGGAGC
GCP18-10129R20-ba2 GTAA.CCTTA CCTAGAGTGA TCTGAGGAGT AGGCTCGTTG CCAGCGGAGC
Consensus .t.aa.ctta c.tagagtga t.tgaggagt aggctcgttg ccagc.gagc
481
530
EMBH44836anti TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
GCP18-5CP418L-Sams TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
GCP18-2CP418L-Wes TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
GCP18-4CP418L-R2000 TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
consel29bal-Drak TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
GCPS18-129Sam-ba2 TAGCTCTCTC CTCC.CCTCA TGAAGCATCT GCTGCACCTG AGACAACCGT
GCPR18-3129R211-ba2 TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GCTGCACCTG AGACAACCGT
GCP18-10129R20-ba2 TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GCTGCACCTG AGACA.CCGT
Consensus tagctctctc ctccgcctca tgaagcatct g.tgcacctg agacaaccgt
531
580
EMBH44836anti GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCP18-5CP418L-Sams GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCP18-2CP418L-Wes GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCP18-4CP418L-R2000 GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
consel29bal-Drak GACGAAACTT TCCGATCACC GCC.CCAGAA TTCGACGCCG CGCATCGGAA
GCPS18-129Sam-ba2 GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCPR18-3129R211-ba2 GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCP18-10129R20-ba2 GACGAAACTT TCCGATCCCC GCC.CCAGAA TTCGACGCCG CGCATCGGAA
Consensus gacgaaactt tccgatcacc gccaccagaa ttcgacgccg cgcatcggaa
581
630
EMBH44836anti GGATCCGAAT CGGGAACTGG AGTGAACCCG AGCGATCCCG GGAGTGCGAC
GCP18-5CP418L-Sams GGATCCGAAT CGGGAACTGG AGTGAACCCG AGCGATCCCG GGAGTGCGAC
GCP18-2CP418L-Wes GGATCCGAAT CGGGAACTGG AGTGAACCCG AGCGATCCCG GGAGTGCGAC
GCP18-4CP418L-R2000 GGATCCGAAT CGGGAACTG. AGTGAACCCG AGCGATCCCG GGAGTGCGAC
consel29bal-Drak GGATCCGAAT CGGGAACTGG AGTGAACCCG AGCGATCCCG GGAGTGCGAC
GCPS18-129Sam-ba2 GGATCCGAAT CGGGAACTGG AGTGAACCAG AGCGATCCCG GGAGTGCGAC
GCPR18-3129R211-ba2 GGATCCGAAT CGG.AACTGG AGTGAACCAG AGCGATCCCG GGAGTGCGAC
GCP18-10129R20-ba2 GGATCCGAAT CGGGAACTGG AGTGAACCAG AGCGATCCCG GGAGTGCGAC
Consensus ggatccgaat cgggaactgg agtgaacc.g agcgatcccg ggagtgcgac

Figure 15 (c)

```
                        631                                                690
          EMBH44836anti GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG
        GCP18-5CP418L-Sams GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG
         GCP18-2CP418L-Wes GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG
      GCP18-4CP418L-R2000 GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG
        consel29bal-Drak GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAA.A GTGGAAGAGG
         GCPS18-129Sam-ba2 GGAGCGTTGG AAAAAGAGAG TGGCACGATT TCGACGAAGA GAGGAAGAGG
      GCPR18-3129R211-ba2 GGAGCGTTGG AAAAAGAGAG TGGCACGATT TCGACGAAGA GAGGAAGAGG
        GCP18-10129R20-ba2 GGAGCGTTGG AAAAAGAGAG TGGCACGATT TCG.CGAAGA GAGGAAGAGG
                 Consensus ggagcg.tgg .aaaagagag tggcacgatt tcgacgaaga g.ggaagagg

                        691                                                740
          EMBH44836anti AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
        GCP18-5CP418L-Sams AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
         GCP18-2CP418L-Wes AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
      GCP18-4CP418L-R2000 AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
        consel29bal-Drak AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
         GCPS18-129Sam-ba2 AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
      GCPR18-3129R211-ba2 AGAGG.TGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAA
        GCP18-10129R20-ba2 AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAA
                 Consensus agagggtggt ggataaactc gcgtatgatc aagttcgtca tcgtcctga.

                        741                                    pSG129antiU  790          800
          EMBH44836anti TGCCGCCATT TTTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG
        GCP18-5CP418L-Sams TGCCGCCATT TTTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG
         GCP18-2CP418L-Wes TGCCGCCATT TTTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG
      GCP18-4CP418L-R2000 TGCCGCCATT TTTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGTG.
        consel29bal-Drak TGCCGCCATT TTTTTTGTCA GGGCGCTCTG .GGCTTAGAA GTTTCCGA..
         GCPS18-129Sam-ba2 TGCCGCCATT CTTGTTCAC. .GGCGCTCTG GGT..... ..........
      GCPR18-3129R211-ba2 TGCCGCC... .......... .......... .......... ..........
        GCP18-10129R20-ba2 TGCC..CAT. CTTGAGCTC. .GG.GCGCGG GCTCACAA.. ..........
                 Consensus tgccgccat. .tt.....c. .gg.gc.c.g ..........  ..........

                        791
          EMBH44836anti TCAATGAAC A GTGACACGAC GAAATGC
        GCP18-5CP418L-Sams TCAATGAAAC AGAAT...TC CGGG...
         GCP18-2CP418L-Wes CCAATGAACA AGATTATTTC CGATG..
      GCP18-4CP418L-R2000 .......... .......... .......
        consel29bal-Drak .......... .......... .......
```

Figure 16

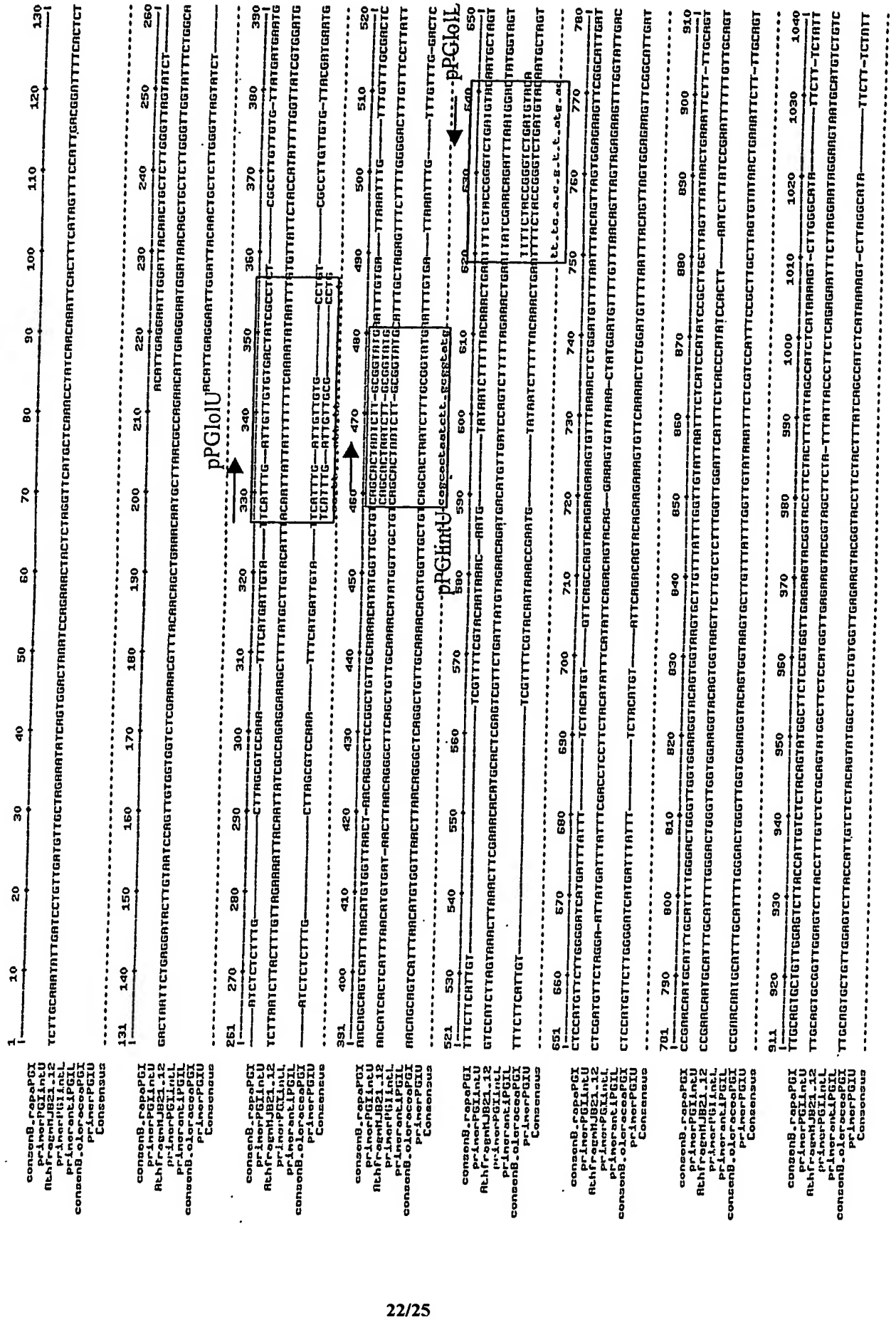

pPGlolU
pPGlolL
pPGHindU
consen8.repaPGX
primerPGIintU
AthFragmMJB21.12
primerPGIintL
primerantiPGIL
consen8.oleraceaPGX
primerPGIU
Consensus

Figure 16 BIS

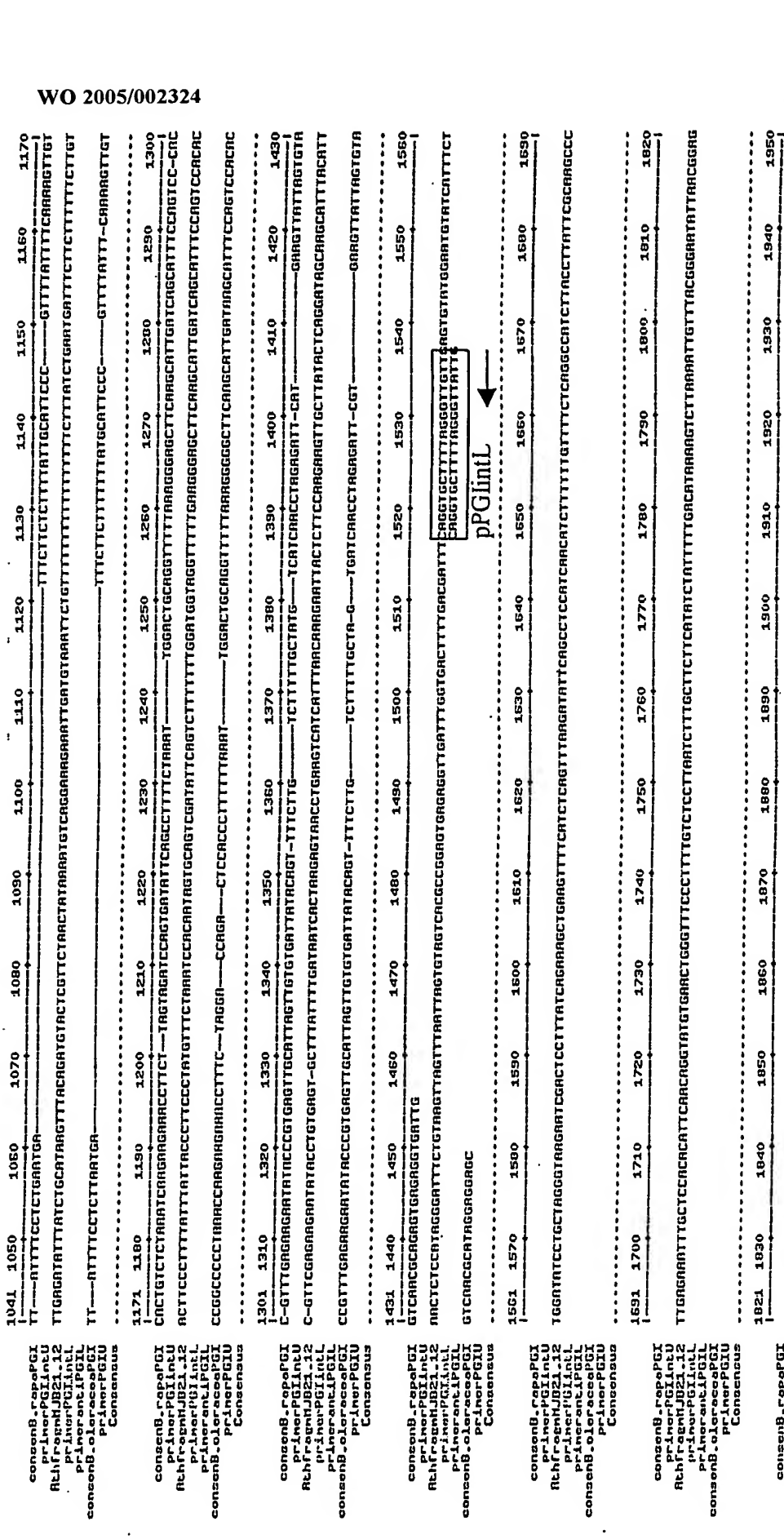
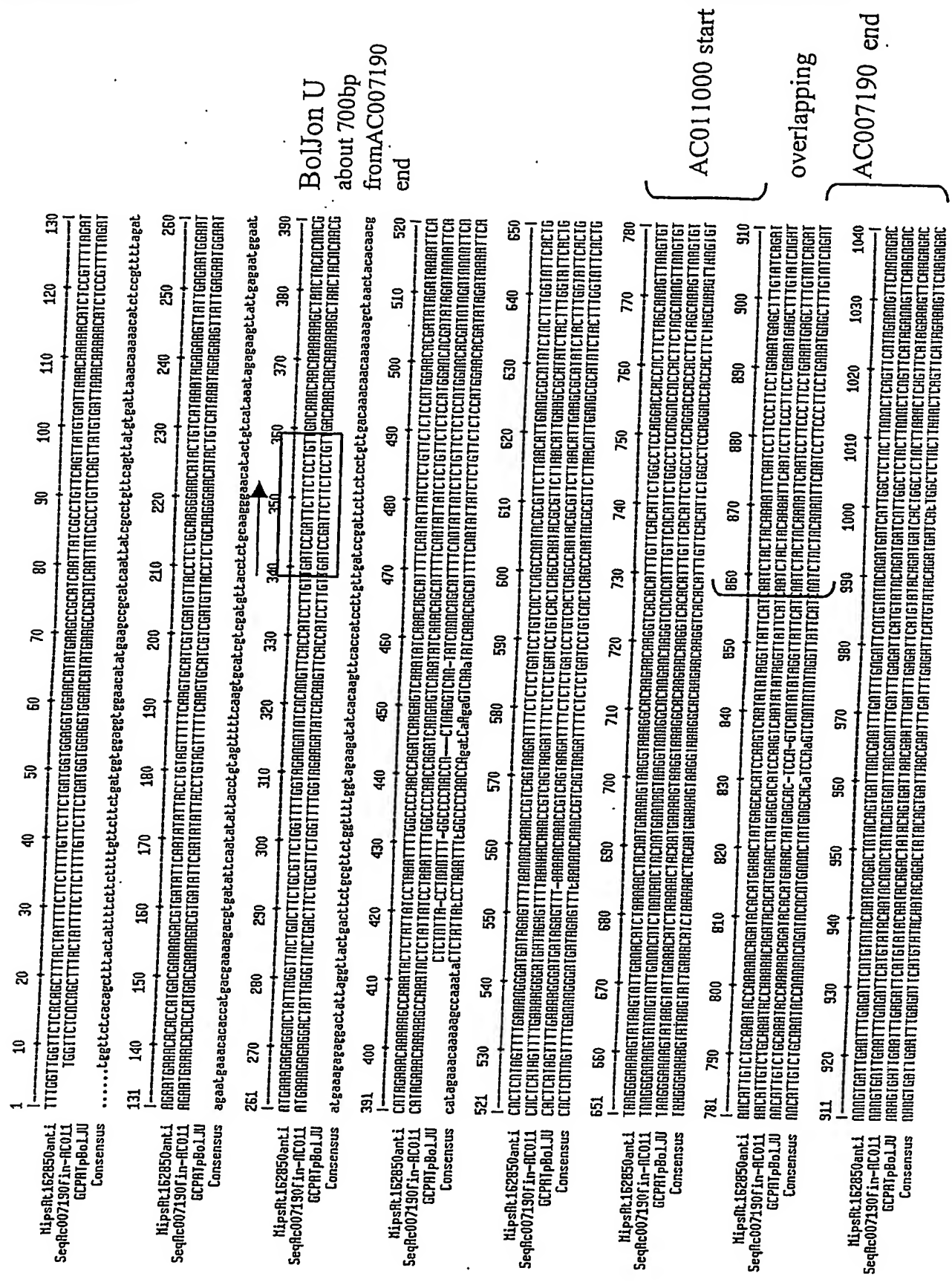


Figure 17


BolJon U about 700bp fromAC007190 end
AC011000 start
overlapping
AC007190 end

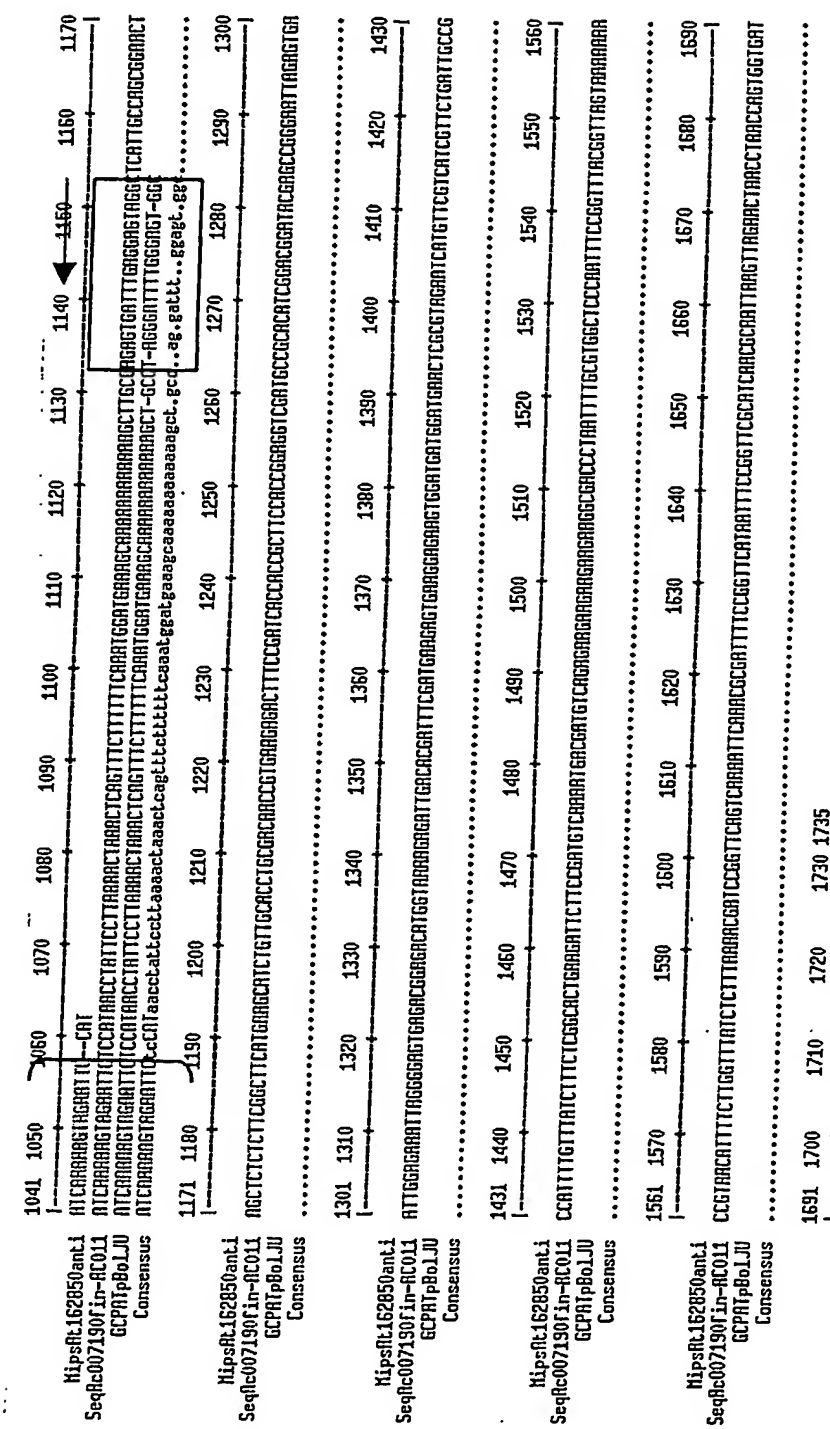



Figure 17 BIS